

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2001, 12:56:11 ; Search time 3039.87 Seconds
(without alignments)
19183.272 Million cell updates/sec

Title: US-09-227-881-3
Perfect score: 6169
Sequence: 1 atcttgcagttactc.....ctgtgcctccatgtcag 6169

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 1022815 seqs, 4726426750 residues

Word size : 8

Total number of hits satisfying chosen parameters: 20439225

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*

```

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
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21: gb_est21:*
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117: gb_est48:*
118: gb_est49:*
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176: gb_est107:*
177: gb_est108:*
178: gb_est109:*

190: gb_est110:*
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193: em_gss_fun:*
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195: em_gss_hum2:*
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197: em_gss_hum4:*
198: em_gss_hum5:*
199: em_gss_hum6:*
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203: em_gss_inv1:*
204: em_gss_inv2:*
205: em_gss_inv3:*
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208: em_gss_pln2:*
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212: em_gss_rod3:*
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248: gb_gss31:*
249: gb_gss32:*
250: gb_gss33:*
251: gb_gss34:*
252: em_gss_inv4:*
253: em_gss_rod6:*
254: em_gss_rod7:*
255: em_gss_rod8:*
256: gb_gss35:*
257: gb_gss36:*
258: gb_gss37:*

pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT	2	
LOCUS	BF726094	429 bp MRNA EST 05-JAN-2001
DEFINITION	bx23h10.y1 Human Iris cDNA (Un-normalized, unamplified): Bx Homo sapiens cDNA clone bx23h10 5', mRNA sequence.	
ACCESSION	BF726094	
VERSION	BF726094.1	GI:12042005
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 429)	
TITLE	Wistow,G.J., Bernstein,S., Behl,A. and Smith,D.	
JOURNAL	NEIBANK: EST analysis and bioinformatics for ocular genomics Invest. Ophthalmol. Vis. Sci. 41 (2000) In press	
COMMENT	Contact: Wistow G Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0076 Email: graeme@helix.nih.gov Plate: 23 row: h column: 10 Seq primer: M13R1 reverse primer (ABI).	
FEATURES	Location/Qualifiers	
source	1..429	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="bx23h10"	
	/clone_1lb="Human Iris cDNA (Un-normalized, unamplified): Bx"	
	/tissue_type="Iris"	
	/dev_stage="Adult"	
	/lab_host="EMDH10B"	
	/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTAGTCTTGAATCGGACGGCGGCC(CT)15-3'. I. Not I blunt end inserts were cloned into the Not I/EcoRV sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."	
BASE COUNT	107 a 129 c 130 g 63 t	
ORIGIN		
Query Match	7.0%; Score 429; DB 166; Length 429;	
Best Local Similarity	100.0%; Prid. No. 3.2e-189;	
Matches 429; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY 5303	cagcgtccagcctctgctcttcctgacctccctcgggtgtggatgtggggccagagacgctc	5442
DB 1	CAGCTGTCACACTGCTGCTTCTGGCTCTCGTGATGTGGGCGCCAGACAGCTC	60
OY 5443	agctcaggaagcccaatgacagagatggcgcgatgcaglataccctcagctggcgcagtc	5502
DB 61	AGCTCAGGAAGGCCCAATGACAGAGTGGCCGATGCACATATTCATTGATGGCCAGTC	120
OY 5503	ccaatgaatccagctcggcccaagacagagccagggccatgtcagtcataactaacagaga	5562
DB 121	CCAAATGAATCCAGCTGCCCAAGCAGACCCAGGCCCATGTCACTCATTAATTACAGA	180
OY 5563	gagacagcagcaccacacagctcttagaccctggggggccacaaagctcagctacgtccctcg	5622

QY	5719	gagagcagctgtaaacacacacagagagctggaagctctacagcaacctctccgag	5718
Db	41	GGGACACAGCTGGAACACCAACGAGAGCTTGAGACAGCTCTACGACCAACCTCTCCGAG	100
QY	5779	acaaagtcagttctgagagagaagaagcagactaaggcaagaanaatgaagattcgcca	5838

Db	101	ACAAGTCAGTCTCTGGAGGAGAGAGAAAGCGACTTAAGGCAGAAATGAGCATCTGGCCA	160
Qy	5839	ggaagcttgaaa	5850
Db	161	GGAGGTTGGAAA	172

[illegible]

REFERENCE
AUTHORS
1 (bases 1 to 593)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt

TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished (2000)
COMMENT	Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 3528
Fax: 301 838 0208
Email: john@elgfr.org
Plate: 70
Seq primer: Reverse.

FEATURES	Location/Qualifiers
source	1. .593

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="MAGE resequences, MAGE"
/note="vector: pbluescriptsm"
BASE COUNT      151 a      142 c      180 g      120 t
ORIGIN

```

Query Match	1.7%	Score 104;	DB 122;	Length 593;
Best Local Similarity	100.0%	Pred. NO.	3.3e-37;	
Best Match 104;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	5837	caagaggttggaagcagcagccagaggtgtagcaagctgtgaagggccagtgtccca	5896
Db	42	CAGGAGGTTGGAAAGCAGCAGCCAGAGGTAGCAAGGCTGAGAAGGGCCAGTGTCCCA	101

Oy 5897 gacccgagacactctcgggctgtgccaccagctccagaagaag 5940
 |||||
 Db 102 GACCCGAGACACTGCTCGGGCTGTGCCACACAGGCTCCAGAGAAG 145

RESULT	5
A0526246/c	
LOCUS	A0526246 420 bp DNA
DEFINITION	HS-5309_B1.B04_Sp6E RPlC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=885 Col=7 Row=D, DNA sequence.
ACCESSION	A0526246
VERSION	A0526246.1 GI:4773566
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS
1 (bases 1 to 420)	
	Mahaffas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel.: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (<http://forresgen.com>). BAC end Web Server: <http://www.hnsc.washington.edu>
Plate: 885 row: D column: 7

High quality sequence stop: 420.

FEATURES	Location/Qualifiers
source	1. .420

```

/jorganism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-885 Col=7 Row=D"
/clone_lib="RPC1-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

```

BASE COUNT	117 a	92 c	109 g	102 f
ORIGIN				

Query Match	1.1%	Score 65	DB 229	Length 420
Best Local Similarity	100.0%	Pred. No.	6e-19	
Matches 65	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1459 ggcctcgttccttgtaactccctgaacctcaaggctatccaccacccctcaagccctctaagaagtgcctcg 1518
|||||
|||
Db 133 ggcttggctttgaaacctgacctcag6gtgatccaccacccctcagacctccttaaagtgcctg 74

QY	1519	gatta	1523
Db	73	GATTA	69

RESULT		6			
A1348766/c					
LOCUS	A1348766	273 bp	mRNA	EST	18-MAR-1999
DEFINITION	t885d4.4.x2 NCI_CGAP_Bn20 Homo sapiens cDNA clone IMAGE:2050830 3 similar to contains Alu repetitive element; mRNA sequence.				
ACCESSION	A1348766				
VERSION	A1348766.1	GI:4085984			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
(bases 1 to 273)	NCI/NINDS-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap .		
	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCAP), Tumor Gene Index			
	Unpublished (1998)			
	Contact: Robert Strausberg, Ph.D.			

JOURNAL COMMENT
Unpublished (1998)
Contact: Robert Strusberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim Jacobson, Ph.D.
cDNA Library Preparation: David B. Krlman, Ph.D.

CDNA library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Insert length: 345 Std Error: 0.00
Seq primer: -400p from Glibco.

FEATURES

source

Location/Qualifiers
1. 273
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2050830"
/clone_lib="NCI-CGAP_Brn20"
/tissue_type="oligodendrogloma"
/dev_stage="adult"
/lab_host="DH108"
/note="Organ: brain; Vector: PAMPI; mRNA made from
oligodendrogloma tissue; cDNA made by oligo-dT priming.
directionally cloned. Size selected on agarose gel.
Average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 119 a 46 c 63 g 45 t
ORIGIN

Query Match 0.9%; Score 58; DB 19; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1326 agctcagtcagctcgcctccaggtcacaacattccctcgtccagccctccgc 1383
|||||
Db 86 AGCTCAGTCAGCTCTGCTCCAGGTCACCAATCTCTGTCACGCTCCGC 29

RESULT 7
AM591614/c 250 bp mRNA EST 22-MAR-2000
LOCUS AM591614
DEFINITION xx15g02.x1 NCI-CGAP-UT1 Homo sapiens cDNA clone IMAGE:2837618 3'
similar to contains Alu repetitive element; contains element MER40
MER40 repetitive element; mRNA sequence.
AM591614
AM591614.1 GI:7278775
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 250)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA library preparation: Life Technologies, Inc.
CDNA library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Image.llnl.gov/image/html/resources.shtml
Seq primer: -400p from Glibco
High quality sequence stop: 239.

FEATURES

source

Location/Qualifiers
1. 250
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2837618"
/clone_lib="NCI-CGAP_UT1"
/tissue_type="well-differentiated endometrial
adenocarcinoma; 7 pooled tumors"
/lab_host="DH108"

/note="Organ: uterus; Vector: PCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
BASE COUNT 88 a 48 c 45 g 69 t
ORIGIN

Query Match 0.9%; Score 57; DB 118; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1476 tgacctaggtgagtcacccaccctcagctcctcaagtgtggtatcacgacatga 1532
|||||
Db 250 TGACCTCAGGTGATCCACCCACCTCAGCCCTCAAGTCTGGATTCACGACATGA 194

RESULT 8
R98218 415 bp mRNA EST 11-SEP-1995
LOCUS R98218
DEFINITION Y975a05.r1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone
IMAGE:201584 5' similar to contains Alu repetitive element; mRNA
sequence.
R98218
R98218.1 GI:983878
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 415)
Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M., Holman
, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston
, R., Williamson, A., Woldmann, P. and Wilson, R.
The WashU-Merkel EST Project
Unpublished (1995)
Contact: Wilison RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 833
High quality sequence stops: 371
Source: IMAGE Consortium, LLNL.
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 833 Std Error: 0.00
Seq primer: M13Rp1
High quality sequence stop: 371.

FEATURES

source

Location/Qualifiers
1. 415
/organism="Homo sapiens"
/db_xref="GDB:3770634"
/db_xref="taxon:9606"
/clone="IMAGE:201584"
/clone_lib="Soares fetal liver spleen INFILS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH108 (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT733D (Pharmacia)
with a modified polylinker; Site:1: Pac I; Site:2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
(5' AACGCAAGATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT733 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 111 a 119 c 78 g 105 t 2 others
ORIGIN

Query Match Best Local Similarity 100.0%; Score 56; DB 188; Length 415; Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1336 agctcaatgcaacctgctccaggttcaagaattctctgtctcagctccc 1381
|||||
Db 54 AGCTCAGTCAACCTCTGCTCCAGGTTCAAGCAATTCCTGTCAGCTCC 109

RESULT 9
AO390434 465 bp DNA GSS 06-MAR-1999
LOCUS CITBI-E1-2554E19.TR CITBI-E1 Homo sapiens genomic clone 2554E19,
DEFINITION DNA sequence.
ACCESSION AO390434.1 GI:4361457
VERSION AO390434
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 465)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department Of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hneetlgr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..465
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2554E19"
/clone_1id="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 109 a 107 c 95 g 151 t 3 others
ORIGIN

Query Match Best Local Similarity 100.0%; Score 56; DB 228; Length 465; Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1336 agctcaatgcaacctgctccaggttcaagaattctctgtctcagctccc 1381
|||||
Db 293 AGCTCAGTCAACCTCTGCTCCAGGTTCAAGCAATTCCTGTCAGCTCC 348

RESULT 10
AM007449 483 bp mRNA EST 09-MAR-2000
LOCUS w55h07.x1 NCI.GCAP_Panl Homo sapiens cDNA clone IMAGE:2511421 3'
DEFINITION similar to contains Alu repetitive element;contains element MER18 repetitive element ;, mRNA sequence.
ACCESSION AM007449
VERSION AM007449.1 GI:5856227
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 483)
AUTHORS NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GCAP clone distribution Information can be found through the I.M.A.G.E. Consortium/JNLN at:
www-bio.llnl.gov/bdrp/image/image.html
Insert Length: 1365 Std Error: 0.00
Seq primer: -40UP from Glbco
High quality sequence stop: 412.
FEATURES
source Location/Qualifiers
1..483
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2511421"
/clone_1id="NCI-GCAP_Panl"
/issue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
BASE COUNT 140 a 99 c 94 g 150 t
ORIGIN

Query Match Best Local Similarity 100.0%; Score 56; DB 110; Length 483; Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1337 gctcactgcaacctgctccaggttcaagaattctctgtctcagctccc 1382
|||||
Db 365 GCTCAGTCAACCTCTGCTCCAGGTTCAAGCAATTCCTGTCAGCTCCG 420

RESULT 11
AO134263 486 bp DNA GSS 23-SEP-1998
LOCUS HS_3047_B1_F02_MF CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=3047 COL=3 Row=L, DNA sequence.
ACCESSION AO134263
VERSION AO134263.1 GI:3525629
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 486)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3047 row: L column: 3
Class: BAC ends

High quality sequence stop: 486.

FEATURES
Location/Qualifiers
1. 486
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="C1047 Col-3 Row-L"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 98 a 126 c 102 g 157 t 3 others

ORIGIN

Query Match 0.9% Score 56; DB 224; Length 486;
Best Local Similarity 100.0%; Pred. No. 9.6e-15;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1327 gctcactgcaacctctgctccaggttcaagcaattctctgtctcagctcccg 1382
|||||

Db 166 gctcactgcaacctctgctccaggttcaagcaattctctgtcagctcccg 221
|||||

RESULT 12
LOCUS AW962388 519 bp mRNA EST 01-JUN-2000
DEFINITION ESTJ14461 MAGE resequences, MAGG Homo sapiens cDNA, mRNA sequence.
ACCESSION AW962388
VERSION AW962388.1 GI:8152224
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 519)
Hegde, P., Ol, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 174
Seq primer: Reverse.
Location/Qualifiers
1. 519
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="MAGE resequences, MAGG"
/note="Vector: pBluescriptSkm"

BASE COUNT 147 a 125 c 132 g 115 t

ORIGIN

Query Match 0.9% Score 56; DB 122; Length 519;
Best Local Similarity 100.0%; Pred. No. 9.5e-15;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1327 gctcactgcaacctctgctccaggttcaagcaattctctgtcagctcccg 1382
|||||

Db 324 gctcactgcaacctctgctccaggttcaagcaattctctgtcagctcccg 269
|||||

RESULT 13
LOCUS AW024656 525 bp mRNA EST 09-MAR-2000
DEFINITION AW7805.x1 NCI-CGAP_K1d3 Homo sapiens cDNA clone IMAGE:2526201 3'
Similar to contains Alu repetitive element; contains element UTR6

repetitive element ;, mRNA sequence.

ACCESSION AW024656
VERSION AW024656.1 GI:5878186
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 525)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Insert length: 1276 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 458.
Location/Qualifiers
1. 525
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="IMAGE:2526201"
/clone_1lb="NCI-CGAP_K1d3"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pTR73D-Pac (Pharmacia) with
a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTR73 vector. mRNA
source: 2 pooled kidneys. Library went through one round
of normalization. Library constructed by Bento Soares and
M. Patricia Bonaldo."

BASE COUNT 149 a 113 c 104 g 159 t

ORIGIN

Query Match 0.9% Score 56; DB 110; Length 525;
Best Local Similarity 100.0%; Pred. No. 9.5e-15;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1327 gctcactgcaacctctgctccaggttcaagcaattctctgtcagctcccg 1382
|||||

Db 362 gctcactgcaacctctgctccaggttcaagcaattctctgtcagctcccg 417
|||||

RESULT 14
LOCUS AV761433 340 bp mRNA EST 19-OCT-2000
DEFINITION AV761433 MDS Homo sapiens cDNA clone MDSBEA08 5', mRNA sequence.
ACCESSION AV761433
VERSION AV761433.1 GI:10919281
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 340)
Gu, J., Zhao, M., Huang, Q., Xu, X., Peng, Y., Song, H., Xiao, H.,
Gu, Y., Li, N., Qian, B., Liu, F., Ou, J., Gao, X., Cheng, Z., Xu, Z., Zeng
L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G.,
Yang, Y., Gao, G., Zhang, Q., Chen, S., Han, Z. and Chen, Z.
Homo sapiens cDNA MDS clones
Unpublished (2000)

COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
Source
1.340
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MDSBEA08"
/clone_1lb="MDS"
/tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/note="Vector: pTRIPlex2; Site_1: sf11A; Site_2: sf11B"

BASE COUNT 96 a 87 c 96 g 61 t

ORIGIN

Query Match 0.9%; Score 55; DB 110; Length 340;
Best Local Similarity 100.0%; Pred. No. 2.9e-14;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1327 gctacgtgcaacctctgcctccaggttcaagcaattctctgtctcagctccc 1381
|||||
Db 228 gcttctgcaacctctgcctccaggttcaagcaattctctgtctcagctccc 174

RESULT 15
BE143811 430 bp mRNA EST 21-JUN-2000
LOCUS MRO-HT0164-021299-011-d07 HT0164 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE143811
ACCESSION BE143811
VERSION BE143811.1 GI:8606535
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 430)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=MRO-HT0164-021
299-011-d07&tl3=1999-12-02&tl4=1)
Seq primer: puc 18 forward
High quality sequence stop: 429.
Location/Qualifiers
1.430
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="HT0164"
/dev_stage="Adult"

FEATURES
Source

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 85 a 121 c 103 g 121 t

ORIGIN

Query Match 0.9%; Score 55; DB 164; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1326 agctcactgcaacctctgcctccaggttcaagcaattctctgtctcagctccc 1380
|||||
Db 95 AGCTCACTGCACACCTGCTCCAGGTTCAAGCAATTCTCTCAGCCTCC 149

Search completed: November 9, 2001, 00:19:58
Job time: 41027 sec

Fri Nov 9 08:40:39 2001

us-09-227-881-3.olg.rst

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